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## Extended Bayesian Model Averaging for Heritability in Twin Studies

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### Abstract

Family studies are often conducted to examine the existence of familial aggregation. Particularly, twin studies can model separately the genetic and environmental contribution. Here we estimate the heritability of quantitative traits via variance components of random-effects in linear mixed models (LMMs). The motivating example was a myopia twin study containing complex nesting data structures: twins and siblings in the same family and observations on both eyes for each individual. Three models are considered for this nesting structure. Our proposal takes into account the model uncertainty in both covariates and model structures via an extended Bayesian model averaging (EBMA) procedure. We estimate the heritability using EBMA under three suggested model structures. When compared with the results under the model with the highest posterior model probability, the EBMA estimate has smaller variation and is slightly conservative. Simulation studies are conducted to evaluate the performance of variance-components estimates, as well as the selections of risk factors, under the correct or incorrect structure. The results indicate that EBMA, with consideration of uncertainties in both covariates and model structures, is robust in model misspecification than the usual Bayesian model averaging (BMA) that considers only uncertainty in covariates selection.

**Key words :** Bayesian model averaging; Boundary Laplace approximation; Heritability; Linear mixed models; Model uncertainty